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~~RAW SEQUENCE LISTING~~

DATE: 11/15/2001

PATENT APPLICATION: US/09/918,568

TIME: 08:54:29

Input Set : A:\11-6-01.sequence listing.txt

Output Set: N:\CRF3\11152001\I918568.raw

ENTERED**SEQUENCE LISTING**

2 (1) GENERAL INFORMATION:

3 (i) APPLICANT: Yoshinobu OKUNO et al.

4 (ii) TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

5 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

6 (iii) NUMBER OF SEQUENCES: 58

7 (iv) CORRESPONDENCE ADDRESS:

8 (A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

9 (B) STREET: 2033 K Street, N.W., #800

10 (C) CITY: Washington

11 (D) STATE: D.C.

12 (E) COUNTRY: U.S.A.

13 (F) ZIP: 20006

14 (v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

16 (B) COMPUTER: IBM Compatible

17 (C) OPERATING SYSTEM: MS-DOS

18 (D) SOFTWARE: Wordperfect 5.1

19 (vi) CURRENT APPLICATION DATA:

C--> 20 (A) APPLICATION NUMBER: US/09/918,568

C--> 21 (B) FILING DATE: 02-Aug-2001

22 (C) CLASSIFICATION:

23 (vii) PRIOR APPLICATION DATA:

24 (A) APPLICATION NUMBER: 09/004,422

25 (B) FILING DATE: January 8, 1998

28 (A) APPLICATION NUMBER: 08/443,862

29 (B) FILING DATE: May 22, 1995

31 (A) APPLICATION NUMBER: 08/229,781

32 (B) FILING DATE: April 19, 1994

34 (A) APPLICATION NUMBER: 08/054,016

35 (B) FILING DATE: April 29, 1993

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Warren M. Cheek, Jr.

38 (B) REGISTRATION NUMBER: 33,367

39 (C) REFERENCE/DOCKET NUMBER:

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 202-721-8200

42 (B) TELEFAX: 202-721-8250

43 (C) TELEX:

44 (2) INFORMATION FOR SEQ ID NO: 1:

45 (i) SEQUENCE CHARACTERISTICS:

46 (A) LENGTH: 5 amino acids

47 (B) TYPE: amino acid

48 (C) STRANDEDNESS: single

49 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

51 (iii) HYPOTHETICAL:

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```

52      (iv) ANTI-SENSE:
53      (v) FRAGMENT TYPE: internal fragment
54      (vi) ORIGINAL SOURCE:
55          (A) ORGANISM:
56          (B) STRAIN:
57          (C) INDIVIDUAL ISOLATE:
58          (D) DEVELOPMENTAL STAGE:
59          (E) HAPLOTYPE:
60          (F) TISSUE TYPE:
61          (G) CELL TYPE:
62          (H) CELL LINE:
63          (I) ORGANELLE:
64      (vii) IMMEDIATE SOURCE:
65          (A) LIBRARY:
66          (B) CLONE:
67      (viii) POSITION IN GENOME:
68          (A) CHROMOSOME/SEGMENT:
69          (B) MAP POSITION:
70          (C) UNITS:
71      (ix) FEATURE:
72          (A) NAME/KEY:
73          (B) LOCATION:
74          (C) IDENTIFICATION METHOD:
75          (D) OTHER INFORMATION:
76      (x) PUBLICATION INFORMATION:
77          (A) AUTHORS:
78          (B) TITLE:
79          (C) JOURNAL:
80          (D) VOLUME:
81          (E) ISSUE:
82          (F) PAGES:
83          (G) DATE:
84          (H) DOCUMENT NUMBER:
85          (I) FILING DATE:
86          (J) PUBLICATION DATE:
C--> 87      (K) RELEVANT RESIDUES IN SEQ ID NO:
88      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
89      Thr Gly Leu Arg Asn
90      1      5
91      (2) INFORMATION FOR SEQ ID NO: 2:
92      (i) SEQUENCE CHARACTERISTICS:
93          (A) LENGTH: 12 amino acids
94          (B) TYPE: amino acid
95          (C) STRANDEDNESS: single
96          (D) TOPOLOGY: linear
97      (ii) MOLECULE TYPE: peptide
98      (iii) HYPOTHETICAL:
99      (iv) ANTI-SENSE:
100      (v) FRAGMENT TYPE: internal fragment

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103      (vi) ORIGINAL SOURCE:
104          (A) ORGANISM:
105          (B) STRAIN:
106          (C) INDIVIDUAL ISOLATE:
107          (D) DEVELOPMENTAL STAGE:
108          (E) HAPLOTYPE:
109          (F) TISSUE TYPE:
110          (G) CELL TYPE:
111          (H) CELL LINE:
112          (I) ORGANELLE:
113      (vii) IMMEDIATE SOURCE:
114          (A) LIBRARY:
115          (B) CLONE:
116      (viii) POSITION IN GENOME:
117          (A) CHROMOSOME/SEGMENT:
118          (B) MAP POSITION:
119          (C) UNITS:
120      (ix) FEATURE:
121          (A) NAME/KEY:
122          (B) LOCATION:
123          (C) IDENTIFICATION METHOD:
124          (D) OTHER INFORMATION:
125      (x) PUBLICATION INFORMATION:
126          (A) AUTHORS:
127          (B) TITLE:
128          (C) JOURNAL:
129          (D) VOLUME:
130          (E) ISSUE:
131          (F) PAGES:
132          (G) DATE:
133          (H) DOCUMENT NUMBER:
134          (I) FILING DATE:
135          (J) PUBLICATION DATE:
C--> 136      (K) RELEVANT RESIDUES IN SEQ ID NO:
137      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
139 Gly Ile Thr Asn Lys Val Asn Ser Val Ile Glu Lys
140  1           5           10
142 (2) INFORMATION FOR SEQ ID NO: 3:
143      (i) SEQUENCE CHARACTERISTICS:
144          (A) LENGTH: 5 amino acids
145          (B) TYPE: amino acid
146          (C) STRANDEDNESS: single
147          (D) TOPOLOGY: linear
148      (ii) MOLECULE TYPE: peptide
149      (iii) HYPOTHETICAL:
150      (iv) ANTI-SENSE:
151      (v) FRAGMENT TYPE: internal fragment
152      (vi) ORIGINAL SOURCE:
153          (A) ORGANISM:

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154          (B) STRAIN:
155          (C) INDIVIDUAL ISOLATE:
156          (D) DEVELOPMENTAL STAGE:
157          (E) HAPLOTYPE:
158          (F) TISSUE TYPE:
159          (G) CELL TYPE:
160          (H) CELL LINE:
161          (I) ORGANELLE:
162      (vii) IMMEDIATE SOURCE:
163          (A) LIBRARY:
164          (B) CLONE:
165      (viii) POSITION IN GENOME:
166          (A) CHROMOSOME/SEGMENT:
167          (B) MAP POSITION:
168          (C) UNITS:
169      (ix) FEATURE:
170          (A) NAME/KEY:
171          (B) LOCATION:
172          (C) IDENTIFICATION METHOD:
173          (D) OTHER INFORMATION:
174      (x) PUBLICATION INFORMATION:
175          (A) AUTHORS:
176          (B) TITLE:
177          (C) JOURNAL:
178          (D) VOLUME:
179          (E) ISSUE:
180          (F) PAGES:
181          (G) DATE:
182          (H) DOCUMENT NUMBER:
183          (I) FILING DATE:
184          (J) PUBLICATION DATE:
C--> 185      (K) RELEVANT RESIDUES IN SEQ ID NO:
186      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
188 Thr Gly Met Arg Asn
189  1      5
191 (2) INFORMATION FOR SEQ ID NO: 4:
192      (i) SEQUENCE CHARACTERISTICS:
193          (A) LENGTH: 12 amino acids
194          (B) TYPE: amino acid
195          (C) STRANDEDNESS: single
196          (D) TOPOLOGY: linear
197      (ii) MOLECULE TYPE: peptide
198      (iii) HYPOTHETICAL:
199      (iv) ANTI-SENSE:
200      (v) FRAGMENT TYPE: internal fragment
201      (vi) ORIGINAL SOURCE:
202          (A) ORGANISM:
203          (B) STRAIN:
204          (C) INDIVIDUAL ISOLATE:

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205      (D) DEVELOPMENTAL STAGE:
206      (E) HAPLOTYPE:
207      (F) TISSUE TYPE:
208      (G) CELL TYPE:
209      (H) CELL LINE:
210      (I) ORGANELLE:
211      (vii) IMMEDIATE SOURCE:
212          (A) LIBRARY:
213          (B) CLONE:
214      (viii) POSITION IN GENOME:
215          (A) CHROMOSOME/SEGMENT:
216          (B) MAP POSITION:
217          (C) UNITS:
218      (ix) FEATURE:
219          (A) NAME/KEY:
220          (B) LOCATION: 9
221          (C) IDENTIFICATION METHOD:
222          (D) OTHER INFORMATION: /note= "Val or Leu"
223      (x) PUBLICATION INFORMATION:
224          (A) AUTHORS:
225          (B) TITLE:
226          (C) JOURNAL:
227          (D) VOLUME:
228          (E) ISSUE:
229          (F) PAGES:
230          (G) DATE:
231          (H) DOCUMENT NUMBER:
232          (I) FILING DATE:
233          (J) PUBLICATION DATE:
C--> 234      (K) RELEVANT RESIDUES IN SEQ ID NO:
235      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
W--> 237 Gln Ile Asn Gly Lys Leu Asn Arg Xaa Ile Glu Lys
238 1      5      10
240 (2) INFORMATION FOR SEQ ID NO: 5:
241      (i) SEQUENCE CHARACTERISTICS:
242          (A) LENGTH: 19 bases
243          (B) TYPE: nucleic acid
244          (C) STRANDEDNESS: single
245          (D) TOPOLOGY: linear
246      (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
247      (iii) HYPOTHETICAL:
248      (iv) ANTI-SENSE:
W--> 249      (v) FRAGMENT TYPE:
250      (vi) ORIGINAL SOURCE:
251          (A) ORGANISM:
252          (B) STRAIN:
253          (C) INDIVIDUAL ISOLATE:
254          (D) DEVELOPMENTAL STAGE:
255          (E) HAPLOTYPE:

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VERIFICATION SUMMARY

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Input Set : A:\11-6-01.sequence listing.txt

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L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:87 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:136 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:185 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:234 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:283 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:249 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5
L:331 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:297 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
L:379 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:345 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7
L:427 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:393 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8
L:476 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:442 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=9
L:524 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:490 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=10
L:572 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:538 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11
L:620 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:586 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12
L:668 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:634 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13
L:716 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:682 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14
L:764 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:730 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15
L:812 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:778 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=16
L:860 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:826 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17
L:908 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:874 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18
L:956 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:922 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19
L:1004 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:970 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20
L:1052 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1018 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:1100 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1066 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22
L:1148 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1114 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23
L:1196 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1162 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24
L:1244 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]

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L:1210 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25
L:1292 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1258 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26
L:1340 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1306 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27
L:1417 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1383 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28
L:1493 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1459 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29
L:1548 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1514 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30
L:1603 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1569 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31
L:1660 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1626 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32
L:1715 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1681 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33
L:1769 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1735 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34
L:1825 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1789 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=35
L:1879 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1845 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=36
L:1933 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1899 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=37
L:1986 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:1952 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=38
L:2039 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2005 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=39
L:2092 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2058 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=40
L:2145 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2111 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=41
L:2198 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2164 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=42
L:2248 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2212 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=43
L:2296 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2262 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=44
L:2344 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2310 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=45
L:2392 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2358 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=46
L:2467 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:2497 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:2500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:2503 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:2506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:2509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46

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L:2555 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2521 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=47
L:2603 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:2569 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=48
L:2617 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=49
L:2683 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=50
L:2777 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=51
L:2825 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=52
L:2873 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=53
L:2921 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=54
L:2964 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54
L:3072 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54